

Applicati n No.: **09/234.028****NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/234,028A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.

- 4 **Misaligned Amino Acid
Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

- 8 **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 10 **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 **Use of <213>Organism
(NEW RULES)** Sequence(s) are missing this mandatory field or its response.

- 12 **Use of <220>Feature
(NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

- 13 **PatentIn ver. 2.0 "bug"** Please do n t use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

1653

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/234,028ADATE: 05/25/1999
TIME: 14:14:43

Input Set: I234028A.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

E--> 1 <110>
E--> 2 <120>
W--> 3 <130>
4 <140> US/09/234,028A
5 <141> 1999-01-20
E--> 6 <160>

*> see item 13 on Error Summary Sheet
for explanation of missing mandatory
items, if file was created
in Patent In 2.0*

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

E--> 7 <210> 2
8 <211> 456
9 <212> PRT
10 <213> Sus sp.
11 <400> 2
12 Met Asn Leu Asp Ile His Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr
13 1 5 10 15
14 Glu Leu Leu Pro Leu Leu Gln Gln Tyr Glu Val Val Arg Leu Asp Asp
15 20 25 30
16 Cys Gly Leu Thr Glu Glu His Cys Lys Asp Ile Gly Ser Ala Leu Arg
17 35 40 45
18 Ala Asn Pro Ser Leu Thr Glu Leu Cys Leu Arg Thr Asn Glu Leu Gly
19 50 55 60
20 Asp Ala Gly Val His Leu Val Leu Gln Gly Leu Gln Ser Pro Thr Cys
21 65 70 75 80
22 Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly
23 85 90 95
24 Cys Gly Val Leu Pro Ser Thr Leu Arg Ser Leu Pro Thr Leu Arg Glu
25 100 105 110
26 Leu His Leu Ser Asp Asn Pro Leu Gly Asp Ala Gly Leu Arg Leu Leu
27 115 120 125
28 Cys Glu Gly Leu Leu Asp Pro Gln Cys His Leu Glu Lys Leu Gln Leu
29 130 135 140
30 Glu Tyr Cys Arg Leu Thr Ala Ala Ser Cys Glu Pro Leu Ala Ser Val
31 145 150 155 160
32 Leu Arg Ala Thr Arg Ala Leu Lys Glu Leu Thr Val Ser Asn Asn Asp
33 165 170 175
34 Ile Gly Glu Ala Gly Ala Arg Val Leu Gly Gln Gly Leu Ala Asp Ser
35 180 185 190
36 Ala Cys Gln Leu Glu Thr Leu Arg Leu Glu Asn Cys Gly Leu Thr Pro
37 195 200 205
38 Ala Asn Cys Lys Asp Leu Cys Gly Ile Val Ala Ser Gln Ala Ser Leu
39 210 215 220

See next page for explanation of error

FYI
✓

Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> &
<223> fields for each sequence which presents at least one n or Xaa.

12107 1 - Please insert
 12117 1 - ~~Sequence Listing~~ *delete - not used under Sequence Rules*
 <212> PRT *this mandatory*
 <213> Rattus sp. *remove identifier and their responses*

<400> 1

Met	Ser	Leu	Asp	Ile	Gln	Cys	Glu	Gln	Leu	Ser	Asp	Ala	Arg	Trp	Thr
1				5					10					15	
Glu	Leu	Leu	Pro	Leu	Ile	Gln	Gln	Tyr	Gln	Val	Val	Arg	Leu	Asp	Asp
			20					25					30		
Cys	Gly	Leu	Thr	Glu	Val	Arg	Cys	Lys	Asp	Ile	Arg	Ser	Ala	Ile	Gln
		35					40					45			
Ala	Asn	Pro	Ala	Leu	Thr	Glu	Leu	Ser	Leu	Arg	Thr	Asn	Glu	Leu	Gly
	50					55					60				
Asp	Ala	Gly	Val	Gly	Leu	Val	Leu	Gln	Gly	Leu	Gln	Asn	Pro	Thr	Cys
65					70					75					80
Lys	Ile	Gln	Lys	Leu	Ser	Leu	Gln	Asn	Cys	Ser	Leu	Thr	Glu	Ala	Gly
				85					90					95	
Cys	Gly	Val	Leu	Pro	Asp	Val	Leu	Arg	Ser	Leu	Ser	Thr	Leu	Arg	Glu
			100					105						110	
Leu	His	Leu	Asn	Asp	Asn	Pro	Leu	Gly	Asp	Glu	Gly	Leu	Lys	Leu	Leu
		115					120					125			
Cys	Glu	Gly	Leu	Arg	Asp	Pro	Gln	Cys	Arg	Leu	Glu	Lys	Leu	Gln	Leu
		130				135					140				
Glu	Tyr	Cys	Asn	Leu	Thr	Ala	Thr	Ser	Cys	Glu	Pro	Leu	Ala	Ser	Val
145					150					155					160
Leu	Arg	Val	Lys	Pro	Asp	Phe	Lys	Glu	Leu	Val	Leu	Ser	Asn	Asn	Asp
				165					170					175	
Phe	His	Glu	Ala	Gly	Ile	His	Thr	Leu	Cys	Gln	Gly	Leu	Lys	Asp	Ser
			180					185					190		
Ala	Cys	Gln	Leu	Glu	Ser	Leu	Lys	Leu	Glu	Asn	Cys	Gly	Ile	Thr	Ser
		195					200					205			
Ala	Asn	Cys	Lys	Asp	Leu	Cys	Asp	Val	Val	Ala	Ser	Lys	Ala	Ser	Leu
		210				215					220				
Gln	Glu	Leu	Asp	Leu	Gly	Ser	Asn	Lys	Leu	Gly	Asn	Thr	Gly	Ile	Ala
225					230					235					240
Ala	Leu	Cys	Ser	Gly	Leu	Leu	Leu	Pro	Ser	Cys	Arg	Leu	Arg	Thr	Leu
				245					250					255	
Trp	Leu	Trp	Asp	Cys	Asp	Val	Thr	Ala	Glu	Gly	Cys	Lys	Asp	Leu	Cys
			260					265					270		
Arg	Val	Leu	Arg	Ala	Lys	Gln	Ser	Leu	Lys	Glu	Leu	Ser	Leu	Ala	Gly
		275					280					285			
Asn	Glu	Leu	Lys	Asp	Glu	Gly	Ala	Gln	Leu	Leu	Cys	Glu	Ser	Leu	Leu

290

295

300

Glu	Pro	Gly	Cys	Gln	Leu	Glu	Ser	Leu	Trp	Val	Lys	Thr	Cys	Ser	Leu
305					310					315					320
Thr	Ala	Ala	Ser	Cys	Pro	His	Phe	Cys	Ser	Val	Leu	Thr	Lys	Asn	Ser
				325					330					335	
Ser	Leu	Phe	Glu	Leu	Gln	Met	Ser	Ser	Asn	Pro	Leu	Gly	Asp	Ser	Gly
			340					345					350		
Val	Val	Glu	Leu	Cys	Lys	Ala	Leu	Gly	Tyr	Pro	Asp	Thr	Val	Leu	Arg
		355					360					365			
Val	Leu	Trp	Leu	Gly	Asp	Cys	Asp	Val	Thr	Asp	Ser	Gly	Cys	Ser	Ser
		370				375					380				
Leu	Ala	Thr	Val	Leu	Leu	Ala	Asn	Arg	Ser	Leu	Arg	Glu	Leu	Asp	Leu
385					390					395					400
Ser	Asn	Asn	Cys	Met	Gly	Asp	Asn	Gly	Val	Leu	Gln	Leu	Leu	Glu	Ser
				405					410					415	
Leu	Lys	Gln	Pro	Ser	Cys	Ile	Leu	Gln	Gln	Leu	Val	Leu	Tyr	Asp	Ile
			420					425					430		
Tyr	Trp	Thr	Asp	Glu	Val	Glu	Asp	Gln	Leu	Arg	Ala	Leu	Glu	Glu	Glu
		435					440					445			
Arg	Pro	Ser	Leu	Arg	Ile	Ile	Ser								
450						455									